



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96722

TO: Sheela Huff
Location: CM1/8B07/8E12
Art Unit: 1642
Sunday, June 22, 2003

Case Serial Number: 830811

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes

WO 0117557

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:05:14 : Search time 1915 Seconds

(without alignments)
273.551 Million cell updates/sec

Title: US-09-830-811-1

Perfect score: 18
Sequence: 1 ggcgcctgttaacagta 18

Scoring table:

IDENTITY:NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_ov:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pi:*
- 9: gb_pi:*
- 10: gb_pi:*
- 11: gb_pi:*
- 12: gb_pi:*
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- 37: gb_pi:*
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- 39: gb_pi:*
- 40: gb_pi:*
- 41: gb_pi:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	2625	6	A83536
2	18	100.0	2625	6	AX093786
3	18	100.0	2625	6	I34433
4	18	100.0	2625	6	I46831
5	18	100.0	2625	6	I55100
6	18	100.0	2625	6	I55100
7	18	100.0	3440	9	BC013609
8	18	100.0	3661	9	HUMOSF4A
9	18	100.0	3712	6	AR034822
10	18	100.0	3712	6	E07382
11	18	100.0	3867	9	HUMOSF4B
12	18	100.0	3914	6	AR034823
13	18	100.0	3914	6	E07383
14	18	100.0	153588	9	AC010533
15	18	100.0	189894	2	AC068656
16	18	100.0	194690	9	AC025763
17	16.4	91.1	3180	10	MUSC11
18	16.4	91.1	3489	10	MUSOSF4
19	16.4	91.1	3581	6	AR034821
20	16.4	91.1	3581	6	E07381
21	16.4	91.1	4127	6	AX306074
22	16.4	91.1	4127	10	MUSC11
23	16.4	91.1	64849	2	AC113037
24	16.4	91.1	106376	9	AL138714
25	16.4	91.1	118327	9	HS048613
26	16.4	91.1	163192	2	AC123048
27	16.4	91.1	170453	9	AC006600
28	16.4	91.1	173556	2	AC074388
29	16.4	91.1	176625	9	AC015977
30	16.4	91.1	176638	2	AL590312
31	16.4	91.1	178549	2	AC109962
32	16.4	91.1	205594	2	AL355372
33	16.4	91.1	207212	2	AL671876
34	16.4	88.9	4520	8	D88669
35	15.4	85.6	345	6	AX144171
36	15.4	85.6	1206	9	AK027308
37	15.4	85.6	1522	9	BC001611
38	15.4	85.6	1695	10	RN056936
39	15.4	85.6	2137	9	AF213968
40	15.4	85.6	2210	9	HS021881
41	15.4	85.6	2213	9	AF152604
42	15.4	85.6	2307	6	AR116594
43	15.4	85.6	3268	1	AF269352
44	15.4	85.6	3268	6	AX144672
45	15.4	85.6	10058	1	AE001050

ALIGNMENTS

RESULT 1
LOCUS A83536
DEFINITION Sequence 1 from Patent WO9849560.
ACCESSION A83536
VERSION A83536.1 GI:6732796
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2625)
AUTHORS MacCallman,C.D. and Stephenson,M.D.
TITLE CADHERIN-11 AS AN INDICATOR OF VIABLE PREGNANCY
JOURNAL PATENT: WO 9849560-A 1 05-NOV-1998
MACCALLMAN COLIN D (CA); STEPHENSON MARY D (CA)

Pred. No. is the number of results predicted by chance to have a

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SOURCE 1.2625 Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 730 a 661 c 675 g 559 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCTTGTAAACAGTA 18
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Db 185 GGGCGCTTGTAAACAGTA 168

RESULT 2
LOCUS AX093786 2625 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1 from Patent WO0117557.
ACCESSION AX093786
VERSION AX093786.1 GI:13510049
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2625)
AUTHORS Brenner, M.B. and Valencia, X.
TITLE Methods and compositions for treatment of inflammatory disease
using cadherin-11 modulating agents
JOURNAL Patent: WO 0117557-A 1 15-MAR-2001;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
FEATURES
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HEIYHNAVPRSNVGTSVIOVTASDADPTGNSAKIVYSLEQSPFSEVAGTGIR
TALPNDRREAKEEYHVIOAKMGHMGISGTRVITTLIDVNDNPKFPQRLYQMS
VSEAAVGEVGVKAKDPDIGNENLYVNTYDGMSEFETITDYPTQGVRIKKP
VDPEERAYSLKYEAAWHIDPKRTISNGFKOTYVKSVEADDEPFTLAPSVIHKEV
OENAACTVYGRYHAKDPDAANSPLRYSIDRTDLDRFTINPEDGFIKTKRLDREE
TAMLNITVFAELIHNHROEAQVVAIRVLDVNDNAKFAAYEGFIESDQTPLSNO
PIYVTSADKDDTPANGPRFISLPEELIHNFTVVRNDONTAGVYARRGDFSRKOD
LYLPIYISDGGIPRMSSTNTLTIRVCCDVGALLSCNAEAYLNLNGSLTGLNLI
ACVILVLYVLEVLIRQKKEPLIVFEEDVREMLITTYDEGGEGEDDEAPADIATL
NPDIINGFIIPRKDIKEPYOMRPLRPAPNSVYVDPIFNTIOEADNDTAPPTYSI
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BASE COUNT 730 a 661 c 675 g 559 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCTTGTAAACAGTA 18
|||||
Db 185 GGGCGCTTGTAAACAGTA 168

RESULT 3
LOCUS I34433 2625 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 57 from patent US 5597725.
ACCESSION I34433

VERSION I34433.1 GI:1825224
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2625)
AUTHORS Suzuki, S.
TITLE Cadherin-specific antibodies and hybridoma cell lines
JOURNAL Patent: US 5597725-A 57 28-JAN-1997;
FEATURES
source Location/Qualifiers
1.2625
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BASE COUNT 730 a 661 c 675 g 559 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 2625;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCTTGTAAACAGTA 18
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Db 185 GGGCGCTTGTAAACAGTA 168

RESULT 4
LOCUS I46831 2625 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 51 from patent US 5639634.
ACCESSION I46831
VERSION I46831.1 GI:2470796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2625)
AUTHORS Suzuki, S.
TITLE Cadherin polynucleotides
JOURNAL Patent: US 5639634-A 51 17-JUN-1997;
FEATURES
source Location/Qualifiers
1.2625
/organism="unknown"
BASE COUNT 730 a 661 c 675 g 559 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 41;
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OY 1 GGGCGCTTGTAAACAGTA 18
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Db 185 GGGCGCTTGTAAACAGTA 168

RESULT 5
LOCUS I55100 2625 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 57 from patent US 5646250.
ACCESSION I55100
VERSION I55100.1 GI:2476303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2625)
AUTHORS Suzuki, S.
TITLE Cadherin polypeptides
JOURNAL Patent: US 5646250-A 57 08-JUL-1997;
FEATURES
source Location/Qualifiers
1.2625
/organism="unknown"
BASE COUNT 730 a 661 c 675 g 559 t
ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTAAACAGTA 18
 |||||
 DB 185 GCGCGCTGTAAACAGTA 168

RESULT 6
 HOMOCA11A/c
 LOCUS Homo sapiens cadherin-11 mRNA, complete cds.
 DEFINITION L34056
 ACCESSION L34056
 VERSION L34056.1 GI:506403
 KEYWORDS cadherin-11.
 SOURCE Homo sapiens fetus brain cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 2625)
 Suzuki, S., Sano, K. and Tanihara, H.
 Diversity of the cadherin family: evidence for eight new cadherins
 in nervous tissue
 JOURNAL Cell Regul. 2 (4), 261-270 (1991)
 MEDLINE 91283540
 PUBMED 2059658
 2 (bases 1 to 2625)
 Tanihara, H., Sano, K., Helmark, R.L., St. John, T. and Suzuki, S.
 Cloning of five cadherins clarifies characteristic domains of
 cadherin extracellular domain and provides further evidence for two
 structurally different types of cadherin
 JOURNAL Cell Adhesion Commun. 2, 15-26 (1994)
 FEATURES
 SOURCE Location/Qualifiers
 1..2625
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="brain"
 /dev_stage="fetus"
 156..2546
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 /citation=[2]
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 /protein_id="AA35622.1"
 /db_xref="GI:506404"

BASE COUNT 730 a 661 c 675 g 559 t

Query Match 100.0%; Score 18; DB 9; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTAAACAGTA 18
 |||||
 DB 185 GCGCGCTGTAAACAGTA 168

RESULT 7
 BC013609/c
 LOCUS Homo sapiens, clone MGC:17193 IMAGE:4183901, mRNA, complete cds.
 DEFINITION BC013609
 ACCESSION BC013609
 VERSION BC013609.1 GI:15488965
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 3440)
 Strausberg, R.
 JOURNAL Submitted (04-SEP-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: villalobedcm.tmc.edu
 Villalob, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

FEATURES
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 /db_xref="taxon:9606"
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BASE COUNT 1055 a 774 c 792 g 819 t

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QY 1 GCGCGCTGTAAACAGTA 18
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 DB 185 GCGCGCTGTAAACAGTA 168

OY 1 GGGCGCTTGTAAACAGTA 18
 DB 204 GGGCGCTTGTAAACAGTA 187

RESULT 8

HUMOSF4A/c

LOCUS Human mRNA for OB-cadherin-1, complete cds. 3661 bp mRNA linear PRI 05-FEB-1999
 DEFINITION D21254
 VERSION D21254.1 GI:575577
 KEYWORDS ost-4; OB-cadherin-1.
 SOURCE Homo sapiens new born osteosarcoma CDNA to mRNA, clone: pKOT170.
 ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

Okazaki, M., Takeshita, S., Kawai, S., Kikuno, R., Tsujimura, A.,

Molecular cloning and characterization of OB-cadherin, a new member

of cadherin family expressed in osteoblasts

J. Biol. Chem. 269 (16), 12092-12098 (1994)

2 (bases 1 to 3661)

Kikuno, R.

Direct Submission

Submitted (21-OCT-1993) Relko Kikuno, Hoechst Japan Ltd., Pharma

Research Labs., 1-3-2 Minami-dai, Kawagoe, Saitama 350-11, Japan

(E-mail: rikuno@dbj.olg.ac.jp, Tel: 0492-43-6149, Fax: 0492-43-2479)

FEATURES

source

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CDS

gene

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 HETYNANVERSVNGSVLYVADPADPTVNSAKLYVETICQYSEVAKQELR
 TALPNDRAKEEYHVIOAKDMGIMGSGTKYITRTIDNDPRFEPQSVQIS
 VSEAAPGEVGVKADPDIGENGILYVNVYDGMESFEITTDDEPMLEAGYIKRP
 VDEETKRAYSLKVEANHIDPKRISNGPRDTYVALAEDDEPMLASVITHEP
 QENNAAGTVVGVAKADPDANSPRISIDHDDDEFEINEDDFITTPPLDRE
 TAVLNTVFAALIHNRHOBAPVPAIRVLDNDAPRFAPEGFCESDQTKPLSNQ
 PVTITADDKDPTANGPRFITSLEPELTHNENFVNRNDNTAGVYARRGSGRQK
 LYLPIVITDGGITPMSSTNTLTIKVCGCDVNGALLSCNNAEYILNAGISGALAIL
 ACYVILVIVLFEVTLNRQKREPLIVEEDVRENITVDDEGGGEDEADLAIIL
 NPQGLNGIPKRDIPKQYMPRGPLRPANSVVDVDFINTRLOEDNDPPAPYDST
 QITGEGRSVAGSLSSLESATYDSDIDYILQMGPRKKLADLYGSDNFTDDDS"

BASE COUNT 1059 a 846 c 883 g 873 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCTTGTAAACAGTA 18
 DB 471 GGGCGCTTGTAAACAGTA 454

RESULT 9
 AR034822/c

LOCUS AR034822 3712 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 3 from patent US 5869638.
 ACCESSION AR034822
 VERSION AR034822.1 GI:5950427
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

AUTHORS

1 (bases 1 to 3712)

Takeshita, S., Okazaki, M., Kawai, S., Tsujimura, A. and Aman, E.

Bone-related cadherin-like protein and process for its production

Patent: US 5869638-A 3 09-FEB-1999;

FEATURES

source

1..3712

/organism="Unknown"

BASE COUNT 1074 a 856 c 897 g 885 t

ORIGIN

OY 1 GGGCGCTTGTAAACAGTA 18
 DB 490 GGGCGCTTGTAAACAGTA 473

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RESULT 10
 LOCUS E07382/c
 DEFINITION cDNA encoding human OSF-4.
 ACCESSION E07382
 VERSION E07382.1 GI:2175521
 KEYWORDS JP 1994122700-A/2.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 3712)

Mamalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Bone-RELATED CADHERIN-LIKE PROTEIN AND ITS PRODUCTION

Patent: JP 1994122700-A 2 06-MAY-1994;

JOURNAL

COMMENT

HOECHST JAPAN LTD

OS

PN

PD

PE

PF

PI

PJ

PK

PL

PM

PN

PO

PP

PQ

PR

PS

PT

PU

PV

PW

PX

PY

PZ

QA

QB

QC

OS Homo sapiens (human)
 PN JP 1994122700-A/2
 PD 06-MAY-1994
 PE 13-JUL-1993 JP 1993172883
 PF 28-AUG-1992 JP 92P 230028
 PI TAKESHITA ATSUSHI, OKAZAKI MAKOTO, KAWAI SHINJI, PI
 TSUJIMURA ATSUSHI,
 PI AMAN EGON
 PC C07K13/00,A61K37/02,A61K39/395,A61K39/395,A61K49/00,
 PC C07K15/14,
 PC C12N15/12,C12P21/02,C12P21/08;
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 CC hypothetical: No;
 CC anti-sense: No;
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FEATURES

source

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BASE COUNT 1074 a 856 c 897 g 885 t

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 490 GGGCGCTTGTAAACAGTA 473

RESULT 11

HUMOSF4B 3867 bp mRNA linear PRI 05-FEB-1999
 LOCUS Human mRNA for OB-cadherin-2, complete cds.
 DEFINITION D21255
 ACCESSION D21255
 VERSION D21255.1 GI:575578
 KEYWORDS osf-4; OB-cadherin-2.
 SOURCE Homo sapiens new born osteosarcoma cDNA to mRNA, clone:PKOT161.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS Okazaki,M., Takeshita,S., Kawai,S., Kikuno,R., Tsujimura,A.,
 Kudo,A. and Amanu,E.
 TITLE Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts
 J. Biol. Chem. 269 (16), 12092-12098 (1994)
 94216322
 2 (bases 1 to 3867)
 Kikuno,R.
 TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1993) Reiko Kikuno, Hoechst Japan Ltd., Pharma
 Research Labs., 1-3-2 Minami-dai, Kawagoe, Saitama 350-11, Japan
 (E-mail:rkikuno@ddi.nig.ac.jp, Tel:0492-43-6149, Fax:0492-43-2479)

FEATURES

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 477..2558
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 /protein_id="BA04799.1"
 /db_xref="GI:1377895"
 /translation="MKENYCLQALVLCMLCHSHAFPERRHRLRSPFHGHEKKE
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 IDKSGNHNKTLNREERAQYTLMAQADVDROTNSAKLYSILEGQPFYEAQGIIR
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 TALPNDRKAEKEHYHVIQAKDMGGMGLSGTQVTTLVDVNDNPKFPOSVYQS
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BASE COUNT 1098 a 905 c 932 g 932 t
 ORIGIN

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QY 1 GGGCGCTTGTAAACAGTA 18
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 Db 506 GGGCGCTTGTAAACAGTA 489

RESULT 12
 AR034823 3914 bp DNA linear PAT 29-SEP-1999
 LOCUS Sequence 5 from patent US 5869638.
 DEFINITION AR034823
 ACCESSION AR034823
 VERSION AR034823.1 GI:5950428
 KEYWORDS

SOURCE

Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 3914)
 Takeshita,S., Okazaki,M., Kawai,S., Tsujimura,A. and Amanu,E.
 TITLE Bone-related cadherin-like protein and process for its production
 JOURNAL Patent: US 5869638-A 5 09-FEB-1999;
 FEATURES Location/Qualifiers
 1..3914
 /organism="unknown"

BASE COUNT

1110 a 916 c 944 g 944 t

QY 1 GGGCGCTTGTAAACAGTA 18
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 Db 520 GGGCGCTTGTAAACAGTA 503

RESULT 13

E07383 3914 bp RNA linear PAT 29-SEP-1997
 LOCUS E07383
 DEFINITION cDNA encoding human OSF-4.
 ACCESSION E07383
 VERSION E07383.1 GI:2175522
 KEYWORDS JP 1994122700-A/3.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 3914)
 Takeshita,A., Okazaki,M., Kawai,S., Tsujimura,A. and Aman,E.
 TITLE BONE-RELATED CADHERIN-LIKE PROTEIN AND ITS PRODUCTION
 JOURNAL Patent: JP 1994122700-A 3 06-MAY-1994;
 HOECHST JAPAN LTD

COMMENT

OS Homo sapiens (human)
 PN JP 1994122700-A/3
 PD 06-MAY-1994
 PF 13-JUL-1993 JP 1993172883
 PR 28-AUG-1992 JP 92P 230028
 PI TAKEISHITA ATSUSHI, OKAZAKI MAKOTO, KAWAI SHINJI, PI
 TSUJIMURA ATSUSHI,
 AMAN EGON
 PC C07K13/00,A61K37/02,A61K39/395,A61K49/00,
 PC C07K15/14,
 PC C12N15/12,C12P21/02,C12P21/08;
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key
 FH Location/Qualifiers
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 /organism="Homo sapiens"
 /cell_type="primary bone cancer" FT

source

1..3914
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 5'UTR 1..490
 CDS 491..2572
 3'UTR 2573..3914.
 Location/Qualifiers

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 /db_xref="taxon:9606"
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 ORIGIN

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGAACAGTA 18
 |||||||
 Db 520 GCGCGCTTGAACAGTA 503

RESULT 14
 AC010533
 LOCUS
 DEFINITION Homo sapiens chromosome 16 clone RP11-22903, complete sequence.
 VERSION AC010533
 KEYWORDS AC010533.6 GI:11386272
 SOURCE HTG.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 153588)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 153588)
 DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 153588)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (28-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 ON NOV 28, 2000 this sequence version replaced g1:9256236.
 COMMENT Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.5.
 SRS Content:
 WI-9802 G05424
 WI-2756 G03521.

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 /chromosome="16"
 /clone="RP11-22903"
 BASE COUNT 48714 a 29627 c 29013 g 46234 t
 ORIGIN

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGAACAGTA 18
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 Db 133378 GCGCGCTTGAACAGTA 133395

RESULT 15
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 LOCUS
 DEFINITION Homo sapiens chromosome 16 clone CTA-186A5, WORKING DRAFT SEQUENCE,
 22 ordered plices.

ACCESSION AC068656
 VERSION AC068656.2 GI:9295747
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
 SOURCE
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 189894)
 DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 189894)
 DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 ON JUL 20, 2000 this sequence version replaced g1:7712105.
 COMMENT -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 1258011
 Center Clone Name: CIT978SKA_186A5

 Summary Statistics
 Consensus quality: 177227 bases at least Q40
 Consensus quality: 185750 bases at least Q30
 Consensus quality: 187169 bases at least Q20
 Estimated insert size: 171860; agarose-fp estimation
 Estimated insert size: 188894; sum-of-contigs estimation
 Quality coverage: 7.12 in Q20 bases; agarose-fp estimation
 Quality coverage: 6.48 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 22 contigs. Gaps between the contigs
 * are represented as runs of 'N'. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 1851: contig of 1851 bp in length
 * 1852 1951: gap of unknown length
 * 1952 3931: contig of 1980 bp in length
 * 3932 4031: gap of unknown length
 * 4032 8525: contig of 4494 bp in length
 * 8526 8626: gap of unknown length
 * 8626 13024: contig of 4399 bp in length
 * 13025 13124: gap of unknown length
 * 13125 14159: contig of 1035 bp in length
 * 14160 14259: gap of unknown length
 * 14260 15936: contig of 1677 bp in length
 * 15937 16036: gap of unknown length
 * 16037 17770: contig of 1734 bp in length
 * 17771 17870: gap of unknown length
 * 17871 18458: contig of 588 bp in length
 * 18459 18558: gap of unknown length
 * 18559 34459: contig of 15901 bp in length
 * 34460 34559: gap of unknown length
 * 34560 35533: contig of 974 bp in length
 * 35534 35633: gap of unknown length
 * 35634 53249: contig of 17616 bp in length
 * 53250 53349: gap of unknown length
 * 53350 55978: contig of 2629 bp in length
 * 55979 56078: gap of unknown length
 * 56079 85774: contig of 28696 bp in length
 * 85775 85874: gap of unknown length
 * 85875 86633: contig of 759 bp in length
 * 86634 86733: gap of unknown length
 * 86734 94931: contig of 8198 bp in length
 * 94932 95031: gap of unknown length


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* 95032 95951: contig of 920 bp in length
* 95952 96051: gap of unknown length
* 96052 138398: contig of 42347 bp in length
* 138398 138499: gap of unknown length
* 138499 143968: contig of 5470 bp in length
* 143968 144069: gap of unknown length
* 144069 152768: contig of 8700 bp in length
* 152768 152869: gap of unknown length
* 152869 153842: contig of 974 bp in length
* 153842 153943: gap of unknown length
* 153943 166638: contig of 12696 bp in length
* 166638 189894: gap of unknown length
* 189894 23156: contig of 23156 bp in length.

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FEATURES

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        /db_xref="taxon:9606"
        /chromosome="16"
        /clone_id="Caltech human BAC library A"

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BASE COUNT 59539 a 37380 c 36768 g 54101 t 2106 others
IGIN

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Query Match

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Best Local Similarity 100.0%; Score 18; DB 2; Length 189894;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGCGGCTGTAAACAGTA 18
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Db 81209 GGCGGCTGTAAACAGTA 81226

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Search completed: June 22, 2003, 08:44:00
Job time : 1921 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:03:44 ; Search time 236 Seconds

(without alignments)
171.763 Million cell updates/sec

Title: US-09-830-811-1

Perfect score: 18
Sequence: 1 ggcgcgtgataacagta 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /N_Geneseq_101002:*

2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

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6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

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13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

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24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18	100.0	18	21	AA53556	Human cadherin-11
2	18	100.0	2625	18	AA785403	Human cadherin-11
3	18	100.0	2625	18	AA761925	Full length human
4	18	100.0	2625	20	AAV83124	Cadherin-11 cDNA.
5	18	100.0	2625	22	AAV55586	Nucleotide sequence
6	18	100.0	3712	15	AA044392	Sequence of human
7	18	100.0	3867	24	ABK35485	Human endometrial
8	18	100.0	3914	15	AA044393	Sequence of human
9	16.4	91.1	3489	22	AA59534	cDNA encoding a mo

C 10	16.4	91.1	3581	15	AA044391	Sequence of murine
C 11	16.4	91.1	4127	24	AB199752	Mouse ischaemic co
C 12	15.4	85.6	302	20	AAV86757	EST clone AX309.
C 13	15.4	85.6	345	22	AA53750	S. epidermidis ope
C 14	15.4	85.6	654	24	AA058777	Human colon cancer
C 15	15.4	85.6	808	22	AAH03710	Human cDNA clone (
C 16	15.4	85.6	880	22	AAK91670	Human cDNA 5'-end
C 17	15.4	85.6	880	22	AAK93833	Human cDNA clone r
C 18	15.4	85.6	1014	24	ABN90907	Staphylococcus epl
C 19	15.4	85.6	1206	22	AAH15306	Human cDNA sequenc
C 20	15.4	85.6	1456	22	AAK94661	Human full-length
C 21	15.4	85.6	2136	22	ABL60305	Human bromo-functi
C 22	15.4	85.6	2307	19	AAV29267	Phosphatidylinositol
C 23	15.4	85.6	2713	22	AAV93435	Human polyomycleot
C 24	15.4	85.6	3268	22	AAH54030	S. epidermidis gen
C 25	15.4	85.6	7053	22	AA526513	Human cDNA encodin
C 26	14.8	82.2	648	24	ABK78301	Bacillus clausii g
C 27	14.8	82.2	1350	24	ABN26266	Human ORFX polynuc
C 28	14.8	82.2	1466	24	ABK93939	Influenza A/Udorn/
C 29	14.8	82.2	1606	21	AAK50109	Arabidopsis thalia
C 30	14.8	82.2	4873	22	AAK91400	Brassica napus BNM
C 31	14.8	82.2	9373	23	AB107021	Drosophila melanog
C 32	14.8	82.2	12505	23	AB107020	Drosophila melanog
C 33	14.4	80.0	60	24	ABK36377	Human spliced tran
C 34	14.4	80.0	279	21	AA54273	Neisseria meningit
C 35	14.4	80.0	483	21	AA54272	Neisseria gonorrhe
C 36	14.4	80.0	483	21	AA54274	Neisseria meningit
C 37	14.4	80.0	825	21	AAK44203	Arabidopsis thalia
C 38	14.4	80.0	1177	21	AAK81778	N. meningitidis pa
C 39	14.4	80.0	1608	21	AAK41747	Human cDNA differe
C 40	14.4	80.0	2619	24	ABK83735	Human cDNA differe
C 41	14.4	80.0	349980	21	AAK21610	N. meningitidis B
C 42	14.4	80.0	1437668	21	AAK81490	Human ovarian canc
C 43	14	77.8	297	24	AB187175	Human p21-like GPC
C 44	14	77.8	474	22	AAH26610	Human nervous syst
C 45	14	77.8	652	22	ABA13441	

ALIGNMENTS

RESULT 1
ID AA53556
AA53556 standard; DNA, 18 BP.

AC AA53556;
22-NOV-2000 (first entry)

DE Human cadherin-11 antisense oligonucleotide OB-1.
Human; cadherin-11; cad-11; cell differentiation; pregnancy termination;
carcinoma; antisense oligonucleotide; ss.

OS Homo sapiens.
XX WO200026236-A2.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-CA01057.
XX PF 30-OCT-1998; 98US-0106258.
XX PR (UYBR-) UNITV BRITISH COLUMBIA.
XX PA MacCallan CD;
XX PI WPI; 2000-365568/31.
XX DR Increasing or decreasing cagII expression or function to modulate
XX PT differentiation or neoplastic transformation of carcinoma cells to
XX PT treat cancers -

XX Claim 11: Page 22: 37pp; English.
 PS
 CC The present sequence is an antisense oligonucleotide for the human
 CC cadherin-11 (cad-11) mRNA. It can be used to reduce the levels of cad-11
 CC expression in cells, which is useful in the treatment of carcinomas,
 CC particularly prostate tumour cells, for modulating the differentiation
 CC of cells, and in the prevention or termination of pregnancy. It is
 CC particularly useful for preventing metastasis of tumour cells.
 SO Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 21; Length 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCTTGTAAACAGTA 18
 DB 1 GGGCGCTTGTAAACAGTA 18

RESULT 2

AAAT85403/C
 ID AAT85403 standard; cDNA; 2625 BP.

AC AAT85403;

DT 03-NOV-1997 (first entry)

DE Human cadherin-11 coding sequence.

KW Human; cadherin; rat; calcium-dependent cell adhesion protein;

KV superfamily; cytoskeleton; eatenin; cancer; ss.

OS Homo sapiens.

Key Location/Qualifiers
 CDS 156..2546
 /*tag= a
 /product= Cadherin-11

US5646250-A.

08-JUL-1997.

17-APR-1992; 9205-0872643.

19-APR-1993; 9305-0049460.

17-APR-1992; 9205-0872643.

01-NOV-1994; 9405-0332638.

(DOHE-) DOHENY EYE INST.

Suzuki S;

WPI; 1997-36297/33.

Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion

Example 2; Column 87-90; 56pp; English.

This sequence encodes human cadherin-11. The invention specifically provides details of human cadherin-5, -8, -11, -12 and -13, and rat cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell adhesion proteins. They are glycosylated integral membrane proteins that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton through eatenins and other cytoskeleton-associated proteins. The novel cadherin proteins may be used in the analysis of the role of cadherins in various cancers. Sequence analysis of the cadherin proteins also allows investigation of the structure and function of

CC cadherin. The cadherin proteins may be isolated by using anti-cadherin
 CC antibodies. These antibodies may also be used to modulate the activity
 CC of cadherin and to determine the tissue specific distribution of cadherin
 CC proteins. Each subclass of cadherins has a unique tissue distribution
 CC pattern.

SO Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 18; Length 2625;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCTTGTAAACAGTA 18
 DB 185 GGGCGCTTGTAAACAGTA 168

RESULT 3

AAAT61925/C
 ID AAT61925 standard; cDNA; 2625 BP.

AC AAT61925;

DT 14-MAY-1997 (first entry)

DE Full length human cadherin-11 cDNA.

KW Ca2+ dependent; cell adhesion protein; foetal; cadherin; rat;

KV brain; human; antibody; purification; determination;

OS Homo sapiens.

Key Location/Qualifiers
 CDS 156..2546
 /*tag= a

US5597725-A.

28-JAN-1997.

17-APR-1992; 9205-0872643.

26-JAN-1994; 9405-0188228.

17-APR-1992; 9205-0872643.

19-APR-1993; 9305-0049460.

(DOHE-) DOHENY EYE INST.

Suzuki S;

WPI; 1997-108328/10.

P-PSDB; AAM13134.

Antibodies to cadherin proteins - useful as cadherin antagonists.

Example 2; Columns 91-96; 59pp; English.

The present sequence encodes full length human cadherin-11, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA was isolated from a foetal brain cDNA library, using probes based on homologous rat cadherin cDNA. Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

SO Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 18; Length 2625;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTTGTAAACAGTA 18
 DB 185 GCGGCGCTTGTAAACAGTA 168

RESULT 4

AAV83124/C
 ID AAV83124 standard; cDNA; 2625 BP.

XX AAV83124;

XX 02-MAR-1999 (first entry)

XX Cadherin-11 cDNA.

XX Cadherin; morphogenesis; calcium-dependent cell adhesion; pregnancy;

XX endometrium; trophoblast; blastocyst; infertility; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 155..2546

XX FT /*tag= a

XX /product= Cadherin-11

XX MO9849560-A1.

XX 05-NOV-1998.

XX 24-APR-1998; 98WO-CA00397.

XX 25-APR-1997; 97CA-2203718.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX MacCallman CD, Stephenson MD;

XX WPI: 1999-024071/02.

XX P-PSDB: AAW85598.

XX Assessing likelihood of successful pregnancy by measuring levels of
 PT cadherin-11 in endometrium - also diagnosis of infertility from low
 PT cadherin levels and increasing cadherin levels by administering
 PT progesterin or cadherin-encoding DNA
 PS
 XX Claim 7: Page 52-53; 63pp; English.

XX The likelihood of establishing and maintaining a pregnancy, blastocyst
 CC implantation or endometrial receptivity are determined by measuring the
 CC level of cadherin-11 mRNA or protein in endometrial cells. A level below
 CC a standard value indicates inability to establish or maintain pregnancy.
 CC Women who are identified as having low level expression of
 CC cadherin-11 in endometrial cells can then be treated with a genetic
 CC construct comprising the cadherin-11 cDNA. The expression of
 CC cadherin-11 from the construct increases fertility and lessens the
 CC likelihood of miscarriage.
 CC Cadherin-11 expression is a better predictor of endometrial response
 CC and receptiveness than conventional analysis of endometrial cell
 CC morphology.
 CC

XX Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

XX Query Match 100.0%; Score 18; DB 20; Length 2625;

XX Best Local Similarity 100.0%; Pred. No. 3.4; 0; Indels 0; Gaps 0;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTTGTAAACAGTA 18

DB 185 GCGGCGCTTGTAAACAGTA 168

RESULT 5
 AAF55586/C

ID AAF55586 standard; DNA; 2625 BP.
 XX
 AC AAF55586;

XX 29-MAY-2001 (first entry)

XX Nucleotide sequence of a human cadherin-11 polypeptide.

XX Human; cadherin-11; inflammatory joint disorder; chronic synovitis;

XX autoimmune disorder; rheumatoid arthritis; arthritis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 156..2546

XX FT /*tag= a

XX /product= "cadherin-11"

XX MO200117557-A1.

XX 15-MAR-2001.

XX 01-SEP-2000; 2000WO-US24101.

XX 03-SEP-1999; 99US-0152456.

XX 13-SEP-1999; 99US-0153490.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

XX Brenner MB, Valencia X;

XX WPI: 2001-235163/24.

XX P-PSDB: AAB67624.

XX Treating inflammatory joint disorders, e.g. chronic synovitis,

XX autoimmune disorders and rheumatoid arthritis, comprises administering

XX a cadherin-11 inhibitor that inhibits the binding of cadherin-11 to its

XX counter receptor

XX Disclosure: Page 78-82; 89pp; English.

XX The present sequence encodes a human cadherin-11 polypeptide.
 CC Cadherin-11 is a transmembrane molecule that, inter alia, mediates
 CC binding of cells to each other through interaction with itself or its
 CC counter-receptors. Agents which inhibit cadherin-11, or which inhibit
 CC the binding of cadherin-11 to a cadherin-11 counter receptor are used
 CC to treat a subject having an inflammatory joint disorder. The method is
 CC useful for treating inflammatory joint disorders, e.g. chronic synovitis,
 CC autoimmune disorders, rheumatoid arthritis, Lyme disease arthritis,
 CC arthritis associated with inflammatory bowel disease or with ankylosing
 CC spondylitis, Reiter's syndrome, or arthritis associated with systemic
 CC lupus erythematosus. The method may also be used for the rational drug
 CC design of new agents capable of modulating an immune system response.
 CC The nucleotide and amino acid sequences of cadherin-11 modulating agents
 CC may be used in computer-based modelling systems to predict the secondary
 CC and tertiary structure of the extracellular domain, and to target a
 CC toxin or a detectable agent to cells which express cadherin-11
 CC counter-receptors or cadherin-11. The antibodies inhibiting the binding
 CC of cadherin-11 to its counter receptor may be used in screening assays
 CC for identifying pharmaceutical lead compounds in molecular libraries.
 CC

XX Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

XX Query Match 100.0%; Score 18; DB 22; Length 2625;

XX Best Local Similarity 100.0%; Pred. No. 3.4; 0; Indels 0; Gaps 0;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTTGTAAACAGTA 18

DB 185 GCGGCGCTTGTAAACAGTA 168

RESULT 6

XX	DE	Human endometrial cancer related gene, CDH11.
XX	XX	
KW	Human: ds; gene; endometrial cancer; differential expression;	
KM	DNA microarray; protein microarray.	
XX	Homo sapiens.	
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XX	MO20020573-A2.	
XX		
XX	07-FEB-2002.	
XX		
XX	31-JUL-2001; 2001MO-US24104.	
PF		
PR	31-JUL-2000; 2000US-221735P.	
XX		
XX	(BGM) BRIGHAM & WOMENS HOSPITAL INC.	
XX		
XX	Mutler GL;	
XX		
XX	WPI: 2002-179967/23.	
DR	P-PSDB: AAU84265.	
XX		
XX		
PT	Diagnosing endometrial cancer comprises determining expression of	
PT	nucleic acid molecules or expression products that are differentially	
PT	expressed in normal and malignant endometrium	
XX		
XX	Claim 1; Page 45-47; 233pp; English.	
XX		
CC	The invention relates to diagnosing endometrial cancer in a subject	
CC	suspected of having endometrial cancer comprising determining the	
CC	expression of a set of nucleic acid molecules or expression products in	
CC	an endometrial sample suspected of being cancerous, where the set of	
CC	nucleic acid molecules comprises at least 2 nucleic acid molecules	
CC	selected from 50 fully defined sequences as given in the specification.	
CC	The nucleic acids are used as an array of at least 2 of the 50	
CC	nucleic acids bound to a solid substrate. Also included is a solid-phase	
CC	protein microarray comprising at least 2 antibodies or its antigen	
CC	binding fragments, that specifically bind at least 2 different	
CC	polypeptides from the 50 fully defined sequences as given in the	
CC	specification, fixed to a solid substrate. The methods and arrays are	
CC	useful for the diagnosis of endometrial cancer, selecting and monitoring	
CC	treatment regimes and identification of lead compounds useful for the	
CC	treatment of endometrial cancer. The present sequence is one of 50	
CC	genes differentially expressed between cancerous and non-cancerous	
CC	samples.	
XX		
SO	Sequence 3867 BP; 1098 A; 905 C; 932 G; 932 T; 0 other;	
Query Match	100.0%; Score 18; DB 24; Length 3867;	
Best Local Similarity	100.0%; Pred. No. 3.5;	
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
07	1 GCGCGCTTGTAAACAGTA 18	
DB	506 GCGCGCTTGTAAACAGTA 489	
RESULT 8		
ID	AA044393/c	
XX	AA044393 standard; cDNA to mRNA; 3914 BP.	
XX		
AC	AA044393;	
XX		
DT	14-SEP-1994 (first entry)	
XX		
DE	Sequence of human OSF-4-2 cDNA.	
XX		
XX	OSF-4-2; cadherin; growth factor; osteogenesis; osteoblast; therapy;	
KW	diagnosis; ss.	
XX		
XX	Homo sapiens.	
XX		

XX	Key	Location/Qualifiers
FT	CDS	491..2569
FT		/tag- a
XX		
PN	EP85801-A.	
XX		
PD	09-MAR-1994.	
XX		
PE	25-AUG-1993:	93EP-0113602.
XX		
PR	28-AUG-1992:	92JP-0230028.
PA	(FARR) HOECHST JAPAN LTD.	
PI	Anann E., Kawai S., Okazaki M., Takeshita S., Tsujimura A;	
DR	WPI: 1994-076152/10.	
DR	P-PDB; AAR49732.	
XX		
XX	New bone related, cadherin-like OSF-4 proteins - for treatment	
XX	and diagnosis of bone metabolic disease, and nucleic acid	
XX	encoding them	
XX		
PS	Claim 3: Page 23-27; 34pp; English.	
CC		
CC	cDNA libraries were constructed from the mouse osteoblastic cell	
CC	line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and	
CC	then as much common DNA as possible removed by hybridisation between	
CC	the 2 libraries. Residual EI-specific DNA was amplified, inserted	
CC	into lambda g10 and screened by plaque hybridisation. A minbank of	
CC	273 E-specific clones was recovered, their inserts amplified and	
CC	used to screen total RNA from both cell types. One clone specific	
CC	for EI was identified and sequenced. The insert from this clone was	
CC	used to screen cDNA prepd. from EI RNA and the longest posn. insert	
CC	cloned in pCEM 112f (+) to give PKO164. This insert was sequenced.	
CC	It encoded the 796 AA mouse precursor protein (AAQ44391/R49730). The	
CC	insert was also used to screen a cDNA bank prepd. from human	
CC	osteosarcoma to identify 2 clones encoding the 2 human precursor	
CC	proteins - OSF-4-1 and OSF-4-2 (AAQ44392/R49731 and AAQ44393/R49732	
CC	respectively).	
XX		
SQ	Sequence 3914 BP; 1105 A; 920 C; 947 G; 942 T; 0 other;	
XX		
XX	Query Match	100.0% Score 18; DB 15; Length 3914;
XX	Best Local Similarity	100.0%; Prod. NO. 3.5;
XX	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GGCGGCTGTGAACAGTA 18	
	520 GGCGGCTGTGAACAGTA 503	
ID	AAFS9534/C	
ID	AAFS9534 standard; CDNA: 3489 BP.	
XX		
XX	AAFS9534;	
DJ	24-APR-2001 (first entry)	
DE		
XX	cdna encoding a mouse PIP-binding protein, OB-cadherin-1.	
XX		
KW	Mouse OB-cadherin-1; murine; prion protein binding protein; PRBP;	
KW	detectable PrP fusion protein; detection; diagnosis; B lymphocyte;	
KW	PrP-Se-associated disorder; prion disease; Creutzfeldt-Jakob disease;	
KW	CJD; Kuru; fatal familial insomnia; scrapie; BSE;	
KW	bovine spongiform encephalopathy; PrP-C-associated disorder;	
KW	cancer; neurodegenerative disorder; immunological disorder;	
KW	abnormal immunoglobulin secretion; lymphoma; multiple myeloma;	
KW	monoclonal gammopathy; B cell-related autoimmune disease;	
KW	myasthenia gravis; rheumatoid arthritis; ss.	
XX	Mus musculus.	

XX FN M0200100235-A1.
 XX PD 04-JAN-2001.
 XX PE 29-JUN-2000: 2000MO-US17927.
 XX PR 29-JUN-1999: 99US-0342426.
 XX PA (UYMC-) UNIV MCGILL.
 XX PR (CAPR-) CAPRION PHARM INC.
 XX P1 Cashman NR, Dodelet V, Paramithiotis E;
 XX DR WPI: 2001-112393/12.
 XX P-PSDB: AAB59534.
 PT Identifying prion protein binding proteins for use in diagnosis, by
 PT treatment of prion-related diseases, neurodegenerative disorders, by
 PT detecting complex formation with detectable prion protein fusion
 PT protein -
 PS Disclosure: Page -: 77pp: English.
 XX The invention relates to a method of identifying a prion protein
 CC binding protein (PrPp). The method comprises contacting a cell or
 CC biological sample with a detectable prion protein (PrP) fusion protein
 CC under conditions that allow complex formation between the fusion protein
 CC and a PrPp, and detecting the complex, enabling the PrPp to be
 CC identified. The invention also relates to a method for identifying a
 CC nucleic acid molecule which encodes PrPp, which comprises providing a
 CC population of cells expressing a pool of nucleic acid molecules, where
 CC the cells do not normally express PrP on their cell surfaces; exposing
 CC the population of cells to detectably labelled PrP; and identifying a
 CC cell which binds the detectably labelled PrP, thereby enabling the
 CC nucleic acid encoding the PrPp to be identified. The invention further
 CC relates to a method of detecting the abnormally folded pathogenic PrP
 CC isoform (PrP-Sc) in a sample using a PrPp identified according to the
 CC invention; a method for screening potential inhibitors of PrP-Sc/PrPp
 CC binding; the use of a PrPp or PrP-binding portion thereof to inhibit
 CC PrP-Sc activity in a mammal or biological sample; the use of a PrPp or
 CC PrP-binding portion thereof to treat a disorder associated with an
 CC undesirable level of interaction between the normally folded PrP-C and
 CC a PrPp in a mammal; and a method of detecting B lymphocytes in a
 CC biological sample using a PrPp. The invention also encompasses fusion
 CC proteins comprising PrP fused to alkaline phosphatase, or a PrPp fused
 CC to alkaline phosphatase. PrPps, or the PrP-binding portions thereof, are
 CC useful for treating a disorder associated with PrP. The disorder may be
 CC a PrP-Sc-related disorder such as Creutzfeldt-Jakob disease (CJD), Kuru,
 CC fatal familial insomnia in humans, scrapie in sheep, and bovine
 CC spongiform encephalopathy (BSE) in cattle. The disorder may also be
 CC one associated with an undesirable level of interaction between the
 CC normally folded PrP-C and a PrPp in a mammal such as cancer,
 CC neurodegenerative disorders, immunological disorders, abnormal
 CC proliferation or secretion of immunoglobulin, lymphoma, multiple
 CC myeloma, monoclonal gammopathy, B cell-related autoimmune diseases,
 CC amyotonia, or rheumatoid arthritis. The present sequence
 CC represents cDNA encoding murine OB-cadherin-1 which was identified
 CC as a moderate affinity PrPp in the invention.
 CC Note: The present sequence is not shown in the specification, but
 CC was obtained from Genbank (accession number D1253).
 XX
 XX Sequence 3489 BP; 1053 A; 763 G; 791 G; 882 T; 0 other;
 Query Match 91.1%; Score 16.4; DB 22; Length 3489;
 Best Local Similarity 94.4%; Pred. No. 27;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 GGGCGCTTGTAAACAGTA 18
 ||| |||||
 299 GGCAGCTTGTAAACAGTA 282

RESULT 10
AA044391/c
ID AA044391 standard; cDNA to mRNA; 3581 BP.
XX
AC AA044391;
XX
14-SEP-1994 (first entry)
XX
Sequence of murine OSF-4 cDNA.
XX
OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
XX diagnosis; ss.
XX
Mus musculus.
XX
Key Location/Qualifiers
FH CDS 284..2671
FT /tag=a
XX
EP585801-A.
XX
09-MAR-1994.
XX
25-AUG-1993; 93EP-0113602.
XX
28-AUG-1992; 92JP-0230028.
XX
(PARH) HOECHST JAPAN LTD.
XX
Amann E, Kawai S, Okazaki M, Takeshita S, Tsujimura A;
XX
WPI: 1994-076152/10.
XX
P-PSDB; AAR49730.
XX
New bone related, cadherin-like OSF-4 proteins - for treatment
XX and diagnosis of bone metabolic disease, and nucleic acid
XX encoding them
XX
Claim 3; Page 13-17; 34pp; English.
XX
CC cDNA libraries were constructed from the mouse osteoblastic cell
CC line MC3T3-E1 and from mouse liver tissue, amplified by PCR, and
CC then as much common DNA as possible removed by hybridisation between
CC the 2 libraries. Residual EI-specific DNA was amplified, inserted
CC into lambda gt10 and screened by plaque hybridisation. A minilink of
CC 273 E-specific clones was recovered, their inserts amplified and
CC used to screen total RNA from both cell types. One clone specific
CC for EI was identified and sequenced. The insert from this clone was
CC used to screen cDNA prepd. from EI RNA and the longest posm. insert
CC cloned in pGEM 112f (+) to give pXOR164. This insert was sequenced;
CC it encoded the 796 AA mouse precursor protein (AA044391/R49730). The
CC insert was also used to screen a cDNA bank prepd. from human
CC osteosarcoma to identify 2 clones encoding the 2 human precursor
CC proteins OSF-4-1 and OSF-4-2 (AA044392/R49731 and AA044393/R49732
CC respectively).
XX
SQ Sequence 3581 BP; 1121 A; 774 C; 800 G; 886 T; 0 other;

Query Match 91.1%; Score 16.4; DB 15; Length 3581;
Best Local Similarity 94.4%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGGCGTTGTAACAGTA 18
DB 313 GCGAGCTTGTAACAGTA 296

RESULT 11
AB199752/c
ID AB199752 standard; cDNA; 4127 BP.
XX
AC AB199752;
XX

DT 07-MAR-2002 (first entry)
XX
XX Mouse ischemic condition related cDNA sequence SEQ ID NO:825.
DE
XX
XX Mouse; ischemia; compressive ischemia; occlusive ischemia;
KW vasospastic ischemia; ischemic condition; ischemic disease; ss.
XX
XX Mus musculus.
XX
XX MO200188188-A2.
XX
XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-JP04192.
XX
XX 18-MAY-2000; 2000JP-0145977.
XX
XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
XX WPI: 2002-034733/04.
XX
XX P-PSDB; ABB57294.
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX expression levels of particular genes defined in the specification or
XX by determining the expression profile of a gene group comprising these
XX genes -
XX
XX Claim 2; Page 2036-2043; 2690pp; English.
XX
XX The present invention describes a method for examining ischemic
XX conditions, comprising measuring the expression levels of particular
XX genes (I) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (I). The method
XX is useful for examining the ischemic condition (e.g. compressive
XX ischemia, occlusive ischemia or vasospastic ischemia) by measuring
XX expression levels of particular genes (AB199202 to AB199912, encoding
XX the protein sequences in ABB57020 to ABB57374) or by determining the
XX expression profile of a gene group comprising these genes. The
XX expression levels or expression profiles produced by these genes are
XX used as an indicator when screening for ischemic condition-improving
XX drugs or therapeutics for ischemic diseases. AB199913 and AB199914
XX represent PCR primers for a mouse ischemic condition related sequence,
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 4127 BP; 1224 A; 889 C; 928 G; 1086 T; 0 other;

Query Match 91.1%; Score 16.4; DB 24; Length 4127;
Best Local Similarity 94.4%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGGCGTTGTAACAGTA 18
DB 445 GCGAGCTTGTAACAGTA 428

RESULT 12
AAV86757/c
ID AAV86757 standard; cDNA; 302 BP.
XX
XX AAV86757;
XX
XX 27-APR-1999 (first entry)
XX
XX EST clone AX309.
XX
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
XX Homo sapiens.
OS

XX XX WO9845435-A2.
XX PN
XX PD 15-OCT-1998.
XX PF 10-APR-1998; 98WO-US06954.
XX PR 10-APR-1997; 97US-0835913.
XX PA (GENM) GENETICS INST INC.
XX PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
XX PI Racie LA, Spaulding V, Treacy M;
XX DR MPI: 1999-070076/06.
XX PT New polynucleotides encoding human secreted proteins - derived from
XX PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
XX PT ovary, pituitary, retina and colon cDNA libraries
XX PT
XX Claim 1: Page 339; 633pp; English.
XX CC This sequence represents an expressed sequence tag (EST), and is a
XX CC polynucleotide of the invention. The polynucleotides of the invention are
XX CC all secreted EST sequences isolated from a variety of human tissue
XX CC sources. The EST sequences and proteins encoded by them are predicted to
XX CC have useful biological activities which would make them suitable for
XX CC treating, preventing or ameliorating medical conditions in humans and
XX CC animals, although no supporting data is given. Suggested activities
XX CC include nutritional activity, immune stimulating or suppressing activity,
XX CC haematopoiesis regulating activity, tissue growth activity,
XX CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX CC therapy. The EST sequences are also stated to be useful for gene
XX CC
XX SQ Sequence 302 BP; 44 A; 89 C; 56 G; 113 T; 0 other;
XX
XX Query Match 85.6%; Score 15.4; DB 20; Length 302;
XX Best Local Similarity 94.1%; Pred. No. 77;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCGGCTGTGAACAGT 17
XX DB 81 GCGGCTGTGAACAGT 65
XX
XX RESULT 13
XX ID AH53750/c
XX AC AH53750 standard; DNA; 345 BP.
XX AC AH53750;
XX DT 03-SEP-2001 (first entry)
XX DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2893.
XX DE
XX KW Staphylococcus epidermidis SRI strain; Infection; diagnosis;
XX KW vaccination; endocarditis; ds.
XX OS Staphylococcus epidermidis.
XX PN WO200134809-AZ.
XX PD 17-MAY-2001.
XX PF 09-NOV-2000; 2000WO-US30782.
XX PR 09-NOV-1999; 99US-0164258.
XX PA (GLAX) GLAXO GROUP LTD.
XX PT

PI Kimmerly WJ;
XX MPI: 2001-316495/33.
XX DR P-PSDB; AAC82900.
XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX PT useful for vaccinating against infections, e.g. endocarditis -
XX PS Claim 8: Page 754-755; 2188pp; English.
XX CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
XX CC (II), given in AAC81454 to AAC83120, from Staphylococcus epidermidis.
XX CC (I) and (II) can have antibacterial activity and therefore can be used
XX CC in vaccination. The nucleic acids (I) may be used to produce the
XX CC S. epidermidis polypeptides (II) via the production of vectors
XX CC containing them which are used to produce hosts cells which express the
XX CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
XX CC used to vaccinate subjects and to raise antibodies against the bacteria.
XX CC The polypeptides may also be used to assay for other inhibitors of their
XX CC activity and therefore identify compounds that may be used for the
XX CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
XX CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
XX CC polynucleotide sequences from the present invention. AAH55091 to
XX CC AAH55098 represent oligonucleotide sequences and primers which are used
XX CC in the exemplification of the present invention.
XX CC N.B. The present invention specifically claims all the polynucleotide
XX CC sequences given in the sequence listing of the present specification,
XX CC however the sequence listing only goes up to SEQ ID NO:4454 so even
XX CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX SQ Sequence 345 BP; 115 A; 64 C; 67 G; 99 T; 0 other;
XX
XX Query Match 85.6%; Score 15.4; DB 22; Length 345;
XX Best Local Similarity 94.1%; Pred. No. 78;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 GCGGCTGTGAACAGTA 18
XX DB 23 GCGGCTGTGAACAGTA 7
XX
XX RESULT 14
XX ID AB058777
XX AC AB058777 standard; cDNA; 654 BP.
XX AC AB058777;
XX DT 02-AUG-2002 (first entry)
XX DE Human colon cancer related nucleotide sequence SEQ ID NO:2472.
XX DE
XX KW Human: colon cancer; cancer; tissue profiling; forensic; mapping;
XX KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX OS Homo sapiens.
XX PN WO200229086-A2.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-US30732.
XX PR 02-OCT-2000; 2000US-237271P.
XX PA (FARB) BAYER CORP.
XX PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
XX PI Thaglingam A, Lewis ME;
XX DR MPI: 2002-426115/45.
XX PT New isolated nucleic acid that is differentially expressed in cancer

PT tissues useful for determining the presence of colon cancer in a cell
or tissue type, and in antisense therapy.

PS Claim 1; Fig 1; 796pp; English.

CC AB06306 to AB060787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. AB078993 to AB079004 represent proteins
CC encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridizes to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence of
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists.

SQ Sequence 654 BP; 199 A; 122 C; 158 G; 168 T; 7 other;

Query Match 85.6%; Score 15.4; DB 24; Length 654;
Best Local Similarity 94.1%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGCGCTGTAAACAGT 17
Db 186 GCGCGCTGTAAACAGT 202

RESULT 15

AAH03710

AAH03710 standard; cDNA; 808 BP.

AC AAH03710;

XX 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:545.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Claim 1; SEQ ID 545; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 808 BP; 265 A; 149 C; 200 G; 191 T; 3 other;

Query Match 85.6%; Score 15.4; DB 22; Length 808;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGCGCTGTAAACAGT 17
Db 123 GCGCGCTGTAAACAGT 139

Search completed: June 22, 2003, 08:11:48
Job time : 240 secs

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:06:44 ; Search time 49 Seconds

(Without alignments)
112.657 Million cell updates/sec

Title: US-09-830-811-1

Perfect score: 18
Sequence: 1 ggcggctgtcaacagta 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.NA:*
1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	2625	1	US-08-188-228-57
2	18	100.0	2625	1	US-08-332-643-51
3	18	100.0	2625	1	US-08-332-638-57
4	18	100.0	3712	2	US-08-738-949-3
5	18	100.0	3914	2	US-08-738-949-5
6	16.4	85.6	1014	2	US-08-738-949-1
7	15.4	85.6	1014	4	US-09-134-001C-370
8	15.4	85.6	2307	3	US-08-942-008-1
9	14.8	82.2	38584	4	US-09-453-702B-50
10	13.8	76.7	336	2	US-08-606-293-3
11	13.8	76.7	336	2	US-08-606-293-7
12	13.8	76.7	1065	3	US-08-875-811-40
13	13.8	76.7	1065	3	US-08-875-811-48
14	13.8	76.7	1074	3	US-08-875-811-44
15	13.8	76.7	1074	3	US-08-875-811-50
16	13.8	76.7	1086	3	US-08-875-811-46
17	13.8	76.7	1137	3	US-08-875-811-42
18	13.8	76.7	1299	2	US-08-125-462-6
19	13.8	76.7	1299	2	US-08-891-848-6
20	13.8	76.7	1320	2	US-08-125-462-3
21	13.8	76.7	1320	2	US-08-891-848-3
22	13.8	76.7	2100	2	US-08-511-485-9
23	13.8	76.7	2691	3	US-09-212-971-9
24	13.8	76.7	2691	3	US-08-800-929A-9
25	13.8	76.7	2691	4	US-09-617-053A-9
26	13.8	76.7	6727	2	US-08-125-462-2
27	13.8	76.7	6727	2	US-08-891-848-2

C 28	13.8	76.7	6799	2	US-08-125-462-5	Sequence 5, Appl
C 29	13.8	76.7	6799	2	US-08-891-848-5	Sequence 5, Appl
C 30	13.8	76.7	6831	2	US-08-609-049A-27	Sequence 27, Appl
C 31	13.8	76.7	6831	4	US-09-170-996-27	Sequence 27, Appl
C 32	13.8	76.7	49136	4	US-09-422-869-1	Sequence 1, Appl
C 33	13.4	74.4	1197	5	PCT-US94-14277-7	Sequence 7, Appl
C 34	13.4	74.4	1566	4	US-08-871-572B-2	Sequence 2, Appl
C 35	13.4	74.4	2055	4	US-09-197-218-1	Sequence 1, Appl
C 36	13.4	74.4	2255	4	US-08-871-572B-3	Sequence 3, Appl
C 37	13.4	74.4	2791	4	US-09-570-367C-1	Sequence 1, Appl
C 38	13.4	74.4	3955	1	US-08-229-515A-14	Sequence 14, Appl
C 39	13.4	74.4	3955	1	US-08-645-865-14	Sequence 1, Appl
C 40	13.4	74.4	4566	2	US-08-465-976A-1	Sequence 1, Appl
C 41	13.4	74.4	4566	2	US-08-982-412-1	Sequence 1, Appl
C 42	13.2	73.3	50000	4	US-09-146-053-4	Sequence 4, Appl
C 43	13.2	73.3	173	1	US-08-435-684A-49	Sequence 49, Appl
C 44	13.2	73.3	173	2	US-08-934-877A-49	Sequence 49, Appl
C 45	13.2	73.3	173	4	US-08-871-678C-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-188-228-57/C
Sequence 57, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188, 228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 2625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-188-228-57
Query Match 100.0%; Score 18; DB 1; Length 2625;
Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
185 GCGCGCTTGTAAACAGTA 168

RESULT 2

US-08-332-643-51/c

Sequence 51, Application US/08332643

Patent No. 5639634

GENERAL INFORMATION:

APPLICANT: SUZUKI, Shinjaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: Street

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/872,643

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5639634and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 2625 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-332-643-51

Query Match

Best Local Similarity 100.0%; Score 18; DB 1; Length 2625;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
185 GCGCGCTTGTAAACAGTA 168

RESULT 3

US-08-332-638-57/c

Sequence 57, Application US/08332638

Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shinjaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 2625 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-332-638-57

Query Match

Best Local Similarity 100.0%; Score 18; DB 1; Length 2625;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
185 GCGCGCTTGTAAACAGTA 168

RESULT 4

US-08-738-349-3/c

Sequence 3, Application US/08738349

Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Amano, Egon

TITLE OF INVENTION: Bone-related cadherin-like protein and

PROCESS for its production

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3712 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Osteosarcoma
FEATURE:
NAME/KEY: CDS
LOCATION: 461..2848
US-08-738-349-3

Query Match 100.0%; Score 18; DB 2; Length 3712;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTTGTAAACAGTA 18
DB 490 GCGGCTTGTAAACAGTA 473

RESULT 5
US-08-738-349-5/C
Sequence 5, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3914 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 491..2569
US-08-738-349-5

Query Match 100.0%; Score 18; DB 2; Length 3914;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTTGTAAACAGTA 18
DB 520 GCGGCTTGTAAACAGTA 503

RESULT 6
US-08-738-349-1/C
Sequence 1, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
FEATURE:
NAME/KEY: CDS
LOCATION: 284..2671
US-08-738-349-1

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 2; Length 3581;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 313 GCGGCGTGTGAACAGTA 18
GCGGCGTGTGAACAGTA 296

RESULT 7

US-09-134-001C-370/c
Sequence 370, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 370
LENGTH: 1014
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-370

Query Match
Best Local Similarity 85.6%; Score 15.4; DB 4; Length 1014;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 2 GCGGCGTGTGAACAGTA 18
GCGGCGTGTGAACAGTA 676

RESULT 8

US-08-942-008-1
Sequence 1, Application US/08942008
Patent No. 6133419
GENERAL INFORMATION:
APPLICANT: Braseimann, Sylvia
TITLE OF INVENTION: Nucleotide Sequences that Encode
TITLE OF INVENTION: Phosphatidylinositol-3' Kinase Associated Proteins and
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,008
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 332,028
REFERENCE/DOCKET NUMBER: ONYX1027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9738
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1928
US-08-942-008-1

Query Match
Best Local Similarity 85.6%; Score 15.4; DB 3; Length 2307;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1153 GCGGCGTGTGAACAGT 17
GCGGCGTGTGAACAGT 1169

RESULT 9

US-09-453-702B-50
Sequence 50, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blatner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plunkett Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.44MB storage
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-Dec-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fatis, Susan K.
REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 1065 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..1065

OTHER INFORMATION: /note="sfvfbmc1uonc"

US-08-875-811-40

Query Match

Best Local Similarity: 76.7%; Score 13.8; DB 3; Length 1065;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGGCTTGTAAACGTA 18
|||||
DB 553 GCGGCTTGTAAATAGTA 537

RESULT 13

US-08-875-811-48/C

Sequence 48, Application US/08875811
Patent No. 6045793

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.

APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: Fatis, Susan K.

US-08-875-811-48

APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:

NAME: Fatis, Susan K.
REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 1065 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..1065

OTHER INFORMATION: /note="sfvfbmc1uonc"

US-08-875-811-48

Query Match

Best Local Similarity: 76.7%; Score 13.8; DB 3; Length 1065;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGGCTTGTAAACGTA 18
|||||
DB 553 GCGGCTTGTAAATAGTA 537

US-08-875-811-44/C

Sequence 44, Application US/08875811
Patent No. 6045793

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.

APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:

NAME: Fatis, Susan K.

US-08-875-811-44

REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1074
OTHER INFORMATION: /note="MetSeroncA87FBE6"
US-08-875-811-44

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 3; Length 1074;
Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGGCTGTAAACAGTA 18
|||||
DB 907 GCGGCTGTAAATAGTA 891

RESULT 15
US-08-875-811-50/C
Sequence 50, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crey LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02568
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fails, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1074
OTHER INFORMATION: /note="MetGluoncFBE6"
US-08-875-811-50

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 3; Length 1074;
Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGGCTGTAAACAGTA 18
|||||
DB 907 GCGGCTGTAAATAGTA 891

Search completed: June 22, 2003, 09:14:29
Job time : 51 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:44:05 ; Search time 142 Seconds
(without alignments)
186.012 Million cell updates/sec

Title: US-09-830-811-1

Perfect score: 18

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Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	3403	12	US-10-044-090-597	Sequence 597, App
2	18	100.0	3867	10	US-09-919-497-5	Sequence 5, App1
3	15.4	85.6	480	9	US-09-918-995-37236	Sequence 37236, A
4	15.4	85.6	7053	10	US-09-764-864-792	Sequence 792, App
5	14.8	82.2	142	10	US-09-878-574-9162	Sequence 9162, App
6	14.8	82.2	207	10	US-09-878-574-12381	Sequence 12381, A
7	14.8	82.2	222	10	US-09-878-574-12500	Sequence 12500, A
8	14.8	82.2	249	10	US-09-878-574-11388	Sequence 11388, A
9	14.8	82.2	473	9	US-09-918-995-10360	Sequence 10360, A
10	14.8	82.2	648	10	US-09-974-300-5592	Sequence 5592, App
11	14.8	82.2	1347	9	US-09-938-842-208	Sequence 208, App
12	14.8	82.2	36584	9	US-10-114-170-50	Sequence 50, App1
13	14.4	80.0	229	10	US-09-878-574-8610	Sequence 8610, App
14	14.4	80.0	383	9	US-09-918-995-6449	Sequence 6449, App
15	14.4	80.0	1069	10	US-09-833-381-1732	Sequence 1732, App
16	14.4	80.0	2804	9	US-10-198-846-10399	Sequence 10399, App
17	14.4	80.0	4084	12	US-10-044-090-221	Sequence 221, App
18	14.4	77.8	297	10	US-09-867-701-10153	Sequence 10153, A
19	14.4	77.8	312	10	US-09-923-876-3656	Sequence 3656, App

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RESULT 2

US-09-919-497-5/c

Sequence 5, Application US/09919497

Patent No. US2002010662A1

GENERAL INFORMATION:

APPLICANT: Muller, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

FILE REFERENCE: B0801/7225

CURRENT APPLICATION NUMBER: US/09/919, 497

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31

ALIGNMENTS

RESULT 1

US-10-044-090-597/c

Sequence 597, Application US/10044090

Patent No. US20020137081A1

GENERAL INFORMATION:

APPLICANT: Olga Bandman

TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

FILE REFERENCE: PA-0028 US

CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT FILING DATE: 2002-01-09

NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL Program

SEQ ID NO 597

LENGTH: 3403

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID NO. US20020137081A1 1256943CBI

US-10-044-090-597

NUMBER OF SEQ ID NOS: 100
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 5
 LENGTH: 3867
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-919-497-5

Query Match 100.0%; Score 18; DB 10; Length 3867;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGCGCTGTGAACAGT 18
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 Db 506 GCGCGCTGTGAACAGTA 489

RESULT 3

US-09-918-995-37236
 Sequence 37236, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-736
 CURRENT APPLICATION NUMBER: US/09/918,995
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 37236
 LENGTH: 480
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(480)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-37236

Query Match 85.6%; Score 15.4; DB 9; Length 480;
 Best Local Similarity 94.1%; Pred. No. 53;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGCGCTGTGAACAGT 17
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 Db 144 GCGCGCTGTGAACAGT 160

RESULT 4

US-09-764-864-792
 Sequence 792, Application US/09764864
 Patent No. US20020132753A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PT23
 CURRENT APPLICATION NUMBER: US/09/764,864
 PRIOR FILING DATE: 2001-01-17
 NUMBER OF SEQ ID NOS: 1792
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 792
 LENGTH: 7053
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (154)
 OTHER INFORMATION: n equals a,t,g, or c
 US-09-764-864-792

Query Match 85.6%; Score 15.4; DB 10; Length 7053;
 Best Local Similarity 94.1%; Pred. No. 79;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGCGCTGTGAACAGT 17
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 Db 1193 GCGCGCTGTGAACAGT 1209

RESULT 5

US-09-878-574-9162/c
 Sequence 9162, Application US/09878574
 Patent No. US20020110548A1
 GENERAL INFORMATION:
 APPLICANT: Byrum, Joseph R.
 APPLICANT: La Rosa, Thomas J.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 Plants
 FILE REFERENCE: 38-21(15401)B
 CURRENT APPLICATION NUMBER: US/09/878,574
 PRIOR FILING DATE: 2001-12-21
 PRIOR APPLICATION NUMBER: 09/333,535
 PRIOR FILING DATE: 1999-06-14
 NUMBER OF SEQ ID NOS: 15775
 SEQ ID NO 9162
 LENGTH: 142
 TYPE: DNA
 ORGANISM: Glycine max
 OTHER INFORMATION: Clone ID: 701102155H1
 US-09-878-574-9162

Query Match 82.2%; Score 14.8; DB 10; Length 142;
 Best Local Similarity 88.9%; Pred. No. 98;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCGCGCTGTGAACAGT 18
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 Db 136 GCGCGCTGTGAACAGTA 119

RESULT 6

US-09-878-574-12381/c
 Sequence 12381, Application US/09878574
 Patent No. US20020110548A1
 GENERAL INFORMATION:
 APPLICANT: Byrum, Joseph R.
 APPLICANT: La Rosa, Thomas J.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 Plants
 FILE REFERENCE: 38-21(15401)B
 CURRENT APPLICATION NUMBER: US/09/878,574
 PRIOR FILING DATE: 2001-12-21
 PRIOR APPLICATION NUMBER: 09/333,535
 PRIOR FILING DATE: 1999-06-14
 NUMBER OF SEQ ID NOS: 15775
 SEQ ID NO 12381
 LENGTH: 207
 TYPE: DNA
 ORGANISM: Glycine max
 OTHER INFORMATION: Clone ID: 701065703H1
 US-09-878-574-12381

Query Match 82.2%; Score 14.8; DB 10; Length 207;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCGCGCTGTGAACAGT 18
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 Db 143 GCGCGCTGTGAACAGTA 126

RESULT 7
US-09-878-574-12500/C
Sequence 12500, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 12500
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701065851H1
US-09-878-574-12500

Query Match 82.2%; Score 14.8; DB 10; Length 222;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGGCTTGTAAACAGTA 18
DB 164 GGAGGCTTGTAAACAGCA 147

RESULT 8
US-09-878-574-11388/C
Sequence 11388, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 11388
LENGTH: 249
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701064387H1
US-09-878-574-11388

Query Match 82.2%; Score 14.8; DB 10; Length 249;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGGCTTGTAAACAGTA 18
DB 167 GGAGGCTTGTAAACAGCA 150

RESULT 9
US-09-918-995-10360/C
Sequence 10360, Application US/09918995
Patent No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hysep, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for windows version 3.0
SEQ ID NO 10360
LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(473)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-10360

Query Match 82.2%; Score 14.8; DB 9; Length 473;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGGCTTGTAAACAGTA 18
DB 377 GGCGGCTTGTAAACAGCA 360

RESULT 10
US-09-974-300-5592
Sequence 5592, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berna, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5592
LENGTH: 648
TYPE: DNA
ORGANISM: Bacillus clausii
US-09-974-300-5592

Query Match 82.2%; Score 14.8; DB 10; Length 648;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCGGCTTGTAAACAGTA 18
DB 536 GGCGGCTTGTAAACAGTA 553

RESULT 11
US-09-938-842A-208/C
Sequence 208, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 208
LENGTH: 1347
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-208

Query Match 82.2%; Score 14.8; DB 9; Length 1347;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGGCTTGTAAACAGTA 18
1073 GCGGCTTGTAAACCGGA 1056

RESULT 12
US-10-114-170-50
Sequence 50, Application US/10114170
Publication No. US20030023075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.,
Burland, Valerie,
Perna, Nicole T.,
Plunkett, Guy,
Weich, Rod
TITLE OF INVENTION: NO. US20030023075A1 Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plunkett Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296,95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38584
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-114-170-50

Query Match 82.2%; Score 14.8; DB 9; Length 38584;

Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCGGCTTGTAAACAGTA 18
36134 GCGGCTGTGAACAGTA 36151

RESULT 13
US-09-878-574-8610/c
Sequence 8610, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.,
APPLICANT: La Rosa, Thomas J.,
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(13401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 8610
LENGTH: 229
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701101435H1
US-09-878-574-8610

Query Match 80.0%; Score 14.4; DB 10; Length 229;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGCTTGTAAACAG 16
Db 77 GCGGCTTGTAAACAG 62

RESULT 14
US-09-918-995-6449/c
Sequence 6449, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6449
LENGTH: 383
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-6449

Query Match 80.0%; Score 14.4; DB 9; Length 383;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGCTTGTAAACAG 16
Db 239 GCGGCTTGTAAACAG 224

RESULT 15
US-09-833-381-1732/c
Sequence 1732, Application US/09833381

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; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1732
; LENGTH: 1069
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1069)
; OTHER INFORMATION: n = A,T,C or G
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Query Match      80.0%; Score 14.4; DB 10; Length 1069;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Perfect score: 18

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41: /cgn2_6/p/ptodata/1/pna/US121.COMB.seq:*
42: /cgn2_6/p/ptodata/1/pna/US122.COMB.seq:*
43: /cgn2_6/p/ptodata/1/pna/US123.COMB.seq:*

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Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-09-830-811-1	Sequence 1, Appl
2	18	100.0	377	US-09-644-871-418	Sequence 4418, Ap
3	18	100.0	420	US-09-293-972-2969	Sequence 2969, A
4	18	100.0	420	US-09-604-939-2969	Sequence 2969, A
5	18	100.0	443	US-09-287-618-2653	Sequence 2653, A
6	18	100.0	492	US-09-824-518-518	Sequence 518, Ap
7	18	100.0	513	US-09-534-857-1848	Sequence 1848, Ap
8	18	100.0	619	US-09-644-871-7428	Sequence 7428, Ap
9	18	100.0	619	US-09-652-124-7882	Sequence 7882, Ap
10	18	100.0	2625	PCT-US02-18947-670	Sequence 670, Ap
11	18	100.0	2625	PCT-US93-03681-57	Sequence 57, Appl
12	18	100.0	2625	US-09-053-3758-1424	Sequence 1424, Ap
13	18	100.0	2625	US-09-403-441-1	Sequence 1, Appl
14	18	100.0	2625	US-09-442-5898-797	Sequence 797, Ap
15	18	100.0	2625	US-09-654-328-1	Sequence 1, Appl
16	18	100.0	2625	US-10-163-818-1	Sequence 1, Appl
17	18	100.0	2625	US-10-172-118-670	Sequence 670, Ap
18	18	100.0	3296	US-09-770-173-2189	Sequence 2189, Ap
19	18	100.0	3296	US-09-770-173-6393	Sequence 6393, Ap
20	18	100.0	3403	US-10-044-090-597	Sequence 597, Ap
21	18	100.0	3403	US-10-084-817-136	Sequence 136, Ap

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 22 18 100.0 3403 70 US-60-260-483-597
c 23 18 100.0 3460 17 US-09-371-108-6588
c 24 18 100.0 3460 25 US-09-644-871-8016
c 25 18 100.0 3460 25 US-09-652-355-9125
c 26 18 100.0 3460 31 US-09-801-833-6588
c 27 18 100.0 3867 1 PCT-US01-24104-5
c 28 18 100.0 3867 1 PCT-US01-24104-5
c 29 18 100.0 3867 1 PCT-US02-08456-485
c 30 18 100.0 3867 34 US-09-919-497-5
c 31 18 100.0 3867 26 US-09-324-185-30389
c 32 18 100.0 4022 25 US-09-644-871-9324
c 33 18 100.0 4022 26 US-09-667-547-1107
c 34 18 100.0 4022 26 US-09-698-012-8524
c 35 18 100.0 4022 27 US-09-698-012-8524
c 36 18 100.0 4022 28 US-09-710-285-1912
c 37 18 100.0 4022 28 US-09-716-990-1643
c 38 18 100.0 4022 29 US-09-721-588-5127
c 39 18 100.0 4022 29 US-09-726-789-4705
c 40 18 100.0 4022 29 US-09-726-789-4705
c 41 18 100.0 4022 29 US-09-726-789-4705
c 42 18 100.0 4022 29 US-09-726-789-4705
c 43 18 100.0 4022 29 US-09-726-789-4705
c 44 18 100.0 4022 29 US-09-726-789-4705
c 45 18 100.0 5232 65 US-60-213-360-4684
18 100.0 5232 71 US-60-278-258-9362

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ALIGNMENTS

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Sequence 597, App
Sequence 6588, Ap
Sequence 8016, Ap
Sequence 9125, Ap
Sequence 9125, Ap
Sequence 6588, Ap
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 45, Appl1
Sequence 30389, A
Sequence 9324, Ap
Sequence 1107, Ap
Sequence 8524, Ap
Sequence 5446, Ap
Sequence 1912, Ap
Sequence 1643, Ap
Sequence 5127, Ap
Sequence 5202, Ap
Sequence 4705, Ap
Sequence 3024, Ap
Sequence 4684, Ap
Sequence 9362, Ap

```

```

RESULT 1
US-09-830-811-1
Sequence 1, Application US/09830811
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: CADHERIN-11 EXPRESSION, AN ASSAY AND TREATMENT FOR CELLULAR
FILE REFERENCE: INVASIVENESS
CURRENT APPLICATION NUMBER: US/09/830,811
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/106,258
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-830-811-1

```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 32; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 1 GGGCGCTTTAAACAGTA 18
1 GGGCGCTTTAAACAGTA 18

```

```

RESULT 2
US-09-644-871-4418/c
Sequence 4418, Application US/09644871
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600 1167-001
CURRENT APPLICATION NUMBER: US/09/644,871
PRIOR FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,059
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FastSeq for Windows Version 4.0

```

```

SEQ ID NO 4418
LENGTH: 377
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(377)
OTHER INFORMATION: n = A,T,C or G
US-09-644-871-4418

```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 25; Length 377;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 278 GGGCGCTTTAAACAGTA 18
1 GGGCGCTTTAAACAGTA 18

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```

RESULT 3
US-09-293-972-29969/c
Sequence 29969, Application US/09293972
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-769
CURRENT APPLICATION NUMBER: US/09/293,972
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 34258
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29969
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-293-972-29969

```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 16; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 380 GGGCGCTTTAAACAGTA 18
1 GGGCGCTTTAAACAGTA 18

```

```

RESULT 4
US-09-904-939-29969/c
Sequence 29969, Application US/09904939
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-769
CURRENT APPLICATION NUMBER: US/09/904,939
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/293,972
NUMBER OF SEQ ID NOS: 34258
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29969
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-904-939-29969

```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 34; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 380 GGGCGCTTTAAACAGTA 18
1 GGGCGCTTTAAACAGTA 18

```

```
RESULT 5
US-09-287-618-26653/c
; Sequence 26653, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26653
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-287-618-26653

Query Match          100.0%; Score 18; DB 16; Length 443;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTGTAAACAGTA 18
   |||||
Db 427 GCGGCGCTGTAAACAGTA 410

RESULT 6
US-09-824-518-5128/c
; Sequence 5128, Application US/09824518
; GENERAL INFORMATION:
; APPLICANT: Geary, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2078-001
; CURRENT APPLICATION NUMBER: US/09/824,518
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/193,436
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10042
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5128
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-518-5128

Query Match          100.0%; Score 18; DB 31; Length 492;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTGTAAACAGTA 18
   |||||
Db 27 GCGGCGCTGTAAACAGTA 10

RESULT 7
US-09-534-857-1848/c
; Sequence 1848, Application US/09534857
; GENERAL INFORMATION:
; APPLICANT: Sellhame, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
```

```
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ADHESION PROTEINS AND L
; FILE REFERENCE: PD-1012 CIP
; CURRENT APPLICATION NUMBER: US/09/534,857
; CURRENT FILING DATE: 2000-03-24
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 8920
; SOFTWARE: PERL Program
; SEQ ID NO 1848
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01314854
US-09-534-857-1848

Query Match          100.0%; Score 18; DB 20; Length 513;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTGTAAACAGTA 18
   |||||
Db 421 GCGGCGCTGTAAACAGTA 404

RESULT 8
US-09-644-871-7428/c
; Sequence 7428, Application US/09644871
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1167-001
; CURRENT APPLICATION NUMBER: US/09/644,871
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,059
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 9739
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7428
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-644-871-7428

Query Match          100.0%; Score 18; DB 25; Length 619;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCTGTAAACAGTA 18
   |||||
Db 520 GCGGCGCTGTAAACAGTA 503

RESULT 9
US-09-652-124-7882/c
; Sequence 7882, Application US/09652124
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Welch, Nadine S.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1179-001
; CURRENT APPLICATION NUMBER: US/09/652,124
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,131
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 9868
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7882
; LENGTH: 619
; TYPE: DNA
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ORGANISM: Homo sapiens
US-09-652-124-7882

Query Match 100.0%; Score 18; DB 25; Length 619;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTAAACAGTA 18
|||||
DB 520 GCGCGCTGTAAACAGTA 503

RESULT 10

PCT-US02-18947-670/c
Sequence 670, Application PC/TUS0218947
GENERAL INFORMATION:
APPLICANT: Rosetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 670
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_001797
DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-670

Query Match 100.0%; Score 18; DB 1; Length 2625;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTAAACAGTA 18
|||||
DB 185 GCGCGCTGTAAACAGTA 168

RESULT 11

PCT-US93-03681-57/c
Sequence 57, Application PC/TUS9303681
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03681
FILING DATE: 19930419
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 2625 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US93-03681-57

Query Match 100.0%; Score 18; DB 1; Length 2625;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTAAACAGTA 18
|||||
DB 185 GCGCGCTGTAAACAGTA 168

RESULT 12

US-09-053-375B-1424/c
Sequence 1424, Application US/09053375B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1424
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo sapiens
US-09-053-375B-1424

Query Match 100.0%; Score 18; DB 14; Length 2625;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTAAACAGTA 18
|||||
DB 185 GCGCGCTGTAAACAGTA 168

RESULT 13

US-09-403-441-1/c
Sequence 1, Application US/09403441
GENERAL INFORMATION:
APPLICANT: MacCallman, Colin D
TITLE OF INVENTION: Cadherin-11 as an Indicator of Viable Pregnancy.
FILE REFERENCE: 27866/34647
CURRENT APPLICATION NUMBER: US/09/403,441
PRIOR APPLICATION NUMBER: PCT/CA98/00397
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: CA 2,203,718
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo sapiens
US-09-403-441-1

Query Match 100.0%; Score 18; DB 18; Length 2625;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 GCGGCTTGTAAACAGTA 18
 |||||
 Db 185 GCGGCTTGTAAACAGTA 168

RESULT 14

US-09-442-589B-797/C
 ; Sequence 797, Application US/09442589B
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenchik, Alex
 ; APPLICANT: Lukashov, Matvey
 ; TITLE OF INVENTION: Human Cardiovascular Array
 ; FILE REFERENCE: CLON-006CIP10
 ; CURRENT APPLICATION NUMBER: US/09/442,589B
 ; CURRENT FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 09/053,375
 ; PRIOR FILING DATE: 1998-03-31
 ; NUMBER OF SEQ ID NOS: 1194
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 797
 ; LENGTH: 2625
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-442-589B-797

Query Match 100.0%; Score 18; DB 18; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 20;

Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 GCGGCTTGTAAACAGTA 18
 |||||
 Db 185 GCGGCTTGTAAACAGTA 168

RESULT 15

US-09-654-328-1/C
 ; Sequence 1, Application US/09654328
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenner, Michael B.
 ; APPLICANT: Valencia, Xavier
 ; TITLE OF INVENTION: Methods and Compositions for Treatment
 ; FILE REFERENCE: B0801/7187/ERP/MAT
 ; CURRENT APPLICATION NUMBER: US/09/654,328
 ; CURRENT FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: US 60/152,456
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: US 60/153,490
 ; PRIOR FILING DATE: 1999-09-13
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 2625
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (156)...(2546)
 US-09-654-328-1

Query Match 100.0%; Score 18; DB 25; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 20;

Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 1 GCGGCTTGTAAACAGTA 18
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 Db 185 GCGGCTTGTAAACAGTA 168

Search completed: June 22, 2003, 10:01:12
 Job time : 2790 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:11:55 : Search time 774 Seconds
(without alignments)
161,805 Million cell updates/sec

Title: US-09-830-811-1

Perfect score: 18

Sequence: 1 ggcgcctgttaaacagta 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 7816976 seqs, 3478802793 residues

Total number of hits satisfying chosen parameters: 15633952

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Pending Patents NA New:*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB_seq.*
- 2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB_seq.*
- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB_seq.*
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- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB_seq.*
- 6: /cgn2_6/ptodata/1/pna/US11_NEW_COMB_seq.*
- 7: /cgn2_6/ptodata/1/pna/US12_NEW_COMB_seq.*
- 8: /cgn2_6/ptodata/1/pna/US13_NEW_COMB_seq.*
- 9: /cgn2_6/ptodata/1/pna/US14_NEW_COMB_seq.*
- 10: /cgn2_6/ptodata/1/pna/US15_NEW_COMB_seq.*
- 11: /cgn2_6/ptodata/1/pna/US16_NEW_COMB_seq.*
- 12: /cgn2_6/ptodata/1/pna/US17_NEW_COMB_seq.*
- 13: /cgn2_6/ptodata/1/pna/US18_NEW_COMB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	201	US-60-455-444-34244	Sequence 34244, A
2	18	100.0	201	US-60-455-444-34245	Sequence 34245, A
3	18	100.0	201	US-60-455-444-34246	Sequence 34246, A
4	18	100.0	201	US-60-455-444-34256	Sequence 34256, A
5	18	100.0	201	US-60-455-444-34257	Sequence 34257, A
6	18	100.0	201	US-60-455-444-34258	Sequence 34258, A
7	18	100.0	201	US-60-455-444-34268	Sequence 34268, A
8	18	100.0	201	US-60-455-444-34284	Sequence 34284, A
9	18	100.0	201	US-60-455-444-34286	Sequence 34286, A
10	18	100.0	201	US-60-465-241-34244	Sequence 34244, A
11	18	100.0	201	US-60-465-241-34245	Sequence 34245, A
12	18	100.0	201	US-60-465-241-34246	Sequence 34246, A
13	18	100.0	201	US-60-465-241-34256	Sequence 34256, A
14	18	100.0	201	US-60-465-241-34257	Sequence 34257, A
15	18	100.0	201	US-60-465-241-34258	Sequence 34258, A
16	18	100.0	201	US-60-465-241-34268	Sequence 34268, A
17	18	100.0	201	US-60-465-241-34284	Sequence 34284, A
18	18	100.0	201	US-60-465-241-34286	Sequence 34286, A
19	18	100.0	201	US-60-465-241-172763	Sequence 172763, A
20	18	100.0	201	US-60-465-241-172766	Sequence 172766, A

ALIGNMENTS

C 21	18	100.0	201	13	US-60-465-241-172912	Sequence 172912, A
C 22	18	100.0	1026	6	US-09-724-676-6128	Sequence 6128, Ap
C 23	18	100.0	1026	6	US-09-724-676A-6128	Sequence 6128, Ap
C 24	18	100.0	2080	10	US-10-170-235-9735	Sequence 9735, Ap
C 25	18	100.0	2080	13	US-60-455-444-2624	Sequence 2624, Ap
C 26	18	100.0	2080	13	US-60-465-241-2624	Sequence 2624, Ap
C 27	18	100.0	2625	9	US-10-342-687-670	Sequence 670, App
C 28	18	100.0	2625	10	US-10-269-909-6	Sequence 6, App1
C 29	18	100.0	3210	6	US-09-724-676-6129	Sequence 6129, Ap
C 30	18	100.0	3210	6	US-09-724-676A-6129	Sequence 6129, Ap
C 31	18	100.0	3661	1	PCT-US03-15711-151	Sequence 151, App
C 32	18	100.0	3661	8	US-10-440-464-151	Sequence 151, App
C 33	18	100.0	3661	9	US-10-240-425-1210	Sequence 1210, App
C 34	18	100.0	3691	10	US-10-170-235-9237	Sequence 9237, Ap
C 35	18	100.0	3691	13	US-60-455-444-2623	Sequence 2623, Ap
C 36	18	100.0	3691	13	US-60-465-241-2623	Sequence 2623, Ap
C 37	18	100.0	3867	1	PCT-US02-14597-22	Sequence 22, App1
C 38	18	100.0	3867	1	PCT-US03-15711-152	Sequence 152, App
C 39	18	100.0	3867	8	US-10-440-464-152	Sequence 152, App
C 40	18	100.0	3867	9	US-10-240-425-1211	Sequence 1211, Ap
C 41	18	100.0	3867	9	US-10-101-510-485	Sequence 485, App
C 42	18	100.0	6536	10	US-10-170-235-10098	Sequence 10098, A
C 43	18	100.0	6536	13	US-60-455-444-2625	Sequence 2625, Ap
C 44	18	100.0	6536	13	US-60-465-241-2625	Sequence 2625, Ap
C 45	18	100.0	122184	13	US-60-465-241-52470	Sequence 52470, A

RESULT 1
US-60-455-444-34244/c
Sequence 34244, Application US/60455444
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34244
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34244

Query Match 100.08; Score 18; DB 13; Length 201;
Best Local Similarity 100.08; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCgcctgttaaacagta 18
Db 44 GGCgcctgttaaacagta 27
|||||

RESULT 2
US-60-455-444-34245/c
Sequence 34245, Application US/60455444
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34245
LENGTH: 201

TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34245

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 201;
Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGTTGTAACAGTA 18
|||||
DB 37 GCGGCGTTGTAACAGTA 20

RESULT 3
US-60-455-444-34246/c
Sequence 34246, Application US/60455444

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01455
CURRENT APPLICATION NUMBER: US/60/455,444

CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34246

LENGTH: 201
TYPE: DNA

ORGANISM: Homo sapiens
US-60-455-444-34246

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 201;
Pred. No. 6.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGTTGTAACAGTA 18
|||||
DB 32 GCGGCGTTGTAACAGTA 15

RESULT 4
US-60-455-444-34256/c
Sequence 34256, Application US/60455444

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01455
CURRENT APPLICATION NUMBER: US/60/455,444

CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34256

LENGTH: 201
TYPE: DNA

ORGANISM: Homo sapiens
US-60-455-444-34256

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 201;
Pred. No. 6.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGTTGTAACAGTA 18
|||||
DB 44 GCGGCGTTGTAACAGTA 27

RESULT 5
US-60-455-444-34257/c
Sequence 34257, Application US/60455444

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01455

CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18

NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 34257
LENGTH: 201

TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34257

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 201;
Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGTTGTAACAGTA 18
|||||
DB 37 GCGGCGTTGTAACAGTA 20

RESULT 6
US-60-455-444-34258/c
Sequence 34258, Application US/60455444

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01455
CURRENT APPLICATION NUMBER: US/60/455,444

CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34258

LENGTH: 201
TYPE: DNA

ORGANISM: Homo sapiens
US-60-455-444-34258

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 201;
Pred. No. 6.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGTTGTAACAGTA 18
|||||
DB 32 GCGGCGTTGTAACAGTA 15

RESULT 7
US-60-455-444-34268/c
Sequence 34268, Application US/60455444

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01455
CURRENT APPLICATION NUMBER: US/60/455,444

CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34268

LENGTH: 201
TYPE: DNA

ORGANISM: Homo sapiens
US-60-455-444-34268

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 201;
Pred. No. 6.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGCGCTTGTAAACAGTA 18
|||||
DB 32 GCGCGCTTGTAAACAGTA 15

RESULT 8
US-60-455-444-34284/C
Sequence 34284, Application US/60455444
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34284
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34284

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
|||||
DB 44 GCGCGCTTGTAAACAGTA 27

RESULT 9
US-60-455-444-34286/C
Sequence 34286, Application US/60455444
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001455
CURRENT APPLICATION NUMBER: US/60/455,444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34286
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-455-444-34286

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
|||||
DB 37 GCGCGCTTGTAAACAGTA 20

RESULT 10
US-60-465-241-34244/C
Sequence 34244, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001468
CURRENT APPLICATION NUMBER: US/60/465,241

CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34244
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34244

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
|||||
DB 44 GCGCGCTTGTAAACAGTA 27

RESULT 11
US-60-465-241-34245/C
Sequence 34245, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34245
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34245

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
|||||
DB 37 GCGCGCTTGTAAACAGTA 20

RESULT 12
US-60-465-241-34246/C
Sequence 34246, Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: C1001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34246
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-465-241-34246

Query Match 100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTTGTAAACAGTA 18
|||||
DB 32 GCGCGCTTGTAAACAGTA 15

RESULT 13
US-60-465-241-34256/c

Sequence 34256, Application US/60465241

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: C1001468

CURRENT APPLICATION NUMBER: US/60/465,241

NUMBER OF SEQ ID NOS: 258418

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 34256

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-60-465-241-34256

Query Match

Best Local Similarity 100.0%; Score 18; DB 13; Length 201;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTGAACAGTA 18

DB 44 GCGCGCTGTGAACAGTA 27

RESULT 14

US-60-465-241-34257/c

Sequence 34257, Application US/60465241

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: C1001468

CURRENT APPLICATION NUMBER: US/60/465,241

NUMBER OF SEQ ID NOS: 258418

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 34257

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-60-465-241-34257

Query Match

Best Local Similarity 100.0%; Score 18; DB 13; Length 201;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTGAACAGTA 18

DB 37 GCGCGCTGTGAACAGTA 20

RESULT 15

US-60-465-241-34258/c

Sequence 34258, Application US/60465241

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: C1001468

CURRENT APPLICATION NUMBER: US/60/465,241

NUMBER OF SEQ ID NOS: 258418

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 34258

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-60-465-241-34258

Query Match

Best Local Similarity 100.0%; Score 18; DB 13; Length 201;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCTGTGAACAGTA 18

DB 32 GCGCGCTGTGAACAGTA 15

Search completed: June 22, 2003, 10:14:19

Job time : 776 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:06:05 ; Search time 1754 Seconds
(without alignments)
166.202 Million cell updates/sec

Title: US-09-830-811-1

Sequence: 1 ggcgcctgttaacagta 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	18	100.0	579 9	AL708659 DKFZp686K
C 2	18	100.0	585 12	BF194811 709303.X
C 3	18	100.0	943 9	AU133055 AU133055
C 4	18	100.0	960 9	AU132966 AU132966
C 5	18	100.0	964 12	BF337900 BF337900
C 6	17	94.4	239 9	AA091280 cclm2408.

7	16.4	91.1	384	10	AM125499
C	9	16.4	451	9	AI465790
C	8	16.4	453	12	BG802493
C	10	16.4	455	10	BB854489
C	11	16.4	479	10	BB854982
C	12	16.4	498	9	AI391334
C	13	16.4	501	9	AA839644
C	14	16.4	509	14	BM934786
C	15	16.4	539	12	BF464456
C	16	16.4	566	10	AM586982
C	17	16.4	569	9	AI118833
C	18	16.4	569	10	BB650583
C	19	16.4	600	12	BG800007
C	20	16.4	600	12	BG808443
C	21	16.4	601	10	BB652650
C	22	16.4	620	10	AM822684
C	23	16.4	623	10	BB619131
C	24	16.4	642	10	BB660181
C	25	16.4	645	10	BB656306
C	26	16.4	650	10	AM210019
C	27	16.4	656	10	BB627470
C	28	16.4	656	13	B1558800
C	29	16.4	659	10	BB622135
C	30	16.4	681	10	AM209556
C	31	16.4	681	10	BB642928
C	32	16.4	689	10	BE198426
C	33	16.4	706	10	BE198551
C	34	16.4	760	17	BB726531
C	35	16.4	776	13	B1734469
C	36	16.4	797	12	BF244442
C	37	16.4	801	9	AU080267
C	38	16.4	834	13	B1689448
C	39	16.4	844	14	BO143991
C	40	16.4	907	14	BO891796
C	41	16.4	926	12	BF179053
C	42	16.4	952	11	AK012880
C	43	16.4	970	14	BO712732
C	44	16.4	1159	14	BO930532
C	45	16.4	1308	11	AK009182

ALIGNMENTS

RESULT 1
AL708659/c 579 bp mRNA linear EST 22-MAR-2002
LOCUS DKFZp686K1153-r1 686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKFZp686K1153 5', mRNA sequence.
ACCESSION AL708659
VERSION AL708659.1 GI:19692014
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 579)
Wambutt,R., Heubner,D., Mewes,W., Well,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Well,B. and Wiemann,S.)
Unpublished (1999)
COMMENT Contact: Wambutt R
MIPS

Am Klopfersplitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No al sequence available.
This clone (DKFZp686K1153) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers
FEATURES

source

1. 579
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp686K1153"
/clone_lib="686 (synonym: h1cc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTRIPLEX2; Site_1: SfilI; Site_2: SfilI;
CDNA collection"

BASE COUNT 122 a 158 c 191 g 107 t 1 others
ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 579;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCTTGTAAACAGTA 18
|||||
468 GGGCGCTTGTAAACAGTA 451

RESULT 2
LOCUS BF194811/c 585 bp mRNA linear EST 03-NOV-2000
DEFINITION 7093h03.x1 NCI-CGAP OV18 Homo sapiens CDNA clone IMAGE:3644020 3'
ACCESSION Similar to TR:015066 Q15066 OB-CADHERIN-2. ; mRNA sequence.
VERSION BF194811.1 GI:11080564
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 585)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
I M A G E Consortium DNA Sequencing by: Washington University
Clone Sequencing Center
Gene distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.llnl.gov
High quality sequence stop: 508.

FEATURES
SOURCE

1. 585
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3644020"
/clone_lib="NCI-CGAP_OV18"
/tissue_type="fibrothecoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pTR73D-Pac (pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand CDNA was primed with a Not I - oligo(dT) primer [5'
TCCTACATCTGAGTCGACGCGCGCCGACATTTTCTTTTCTTTT 3'];
double-stranded CDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTR73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo.
BASE COUNT 118 a 167 c 193 g 107 t
ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCTTGTAAACAGTA 18
|||||
504 GGGCGCTTGTAAACAGTA 487

RESULT 3
LOCUS AU133055/c 943 bp mRNA linear EST 01-AUG-2002
DEFINITION AU133055 NT2RP4 Homo sapiens CDNA clone NT2RP4001171 5', mRNA
sequence.
ACCESSION AU133055
VERSION AU133055.1 GI:10993594
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 943)
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J.,
Nishikawa, T., Nakamura, T., Nagai, T., Sugano, S., Masuho, Y. and
Isogai, T.
HRI human CDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T., Sugano
, S., Masuho, Y., Isogai, T.)
Unpublished (2000).
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3875
Fax: 81-438-52-3886
Email: genomics@hri.co.jp
HRI Human CDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; CDNA library construction; Department of Helix
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
SOURCE
1. 943
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP4001171"
/clone_lib="NT2RP4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction."
BASE COUNT 211 a 250 c 295 g 182 t 5 others
ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 943;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGCGCTTGTAAACAGTA 18
|||||
509 GGGCGCTTGTAAACAGTA 492

RESULT 4
LOCUS AU132966/c 960 bp mRNA linear EST 01-AUG-2002
DEFINITION AU132966 NT2RP4 Homo sapiens CDNA clone NT2RP4000986 5', mRNA
sequence.
ACCESSION AU132966
VERSION AU132966.1 GI:10993505
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 960)
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J.,

TITLE

Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuko, Y. and
Isogai, T.
HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T., Sugano
S., Masuko, Y., Isogai, T.)
Unpublished (2000)

JOURNAL
COMMENT

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HRI human cDNA project: 5'-63'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 960

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="NT2RP400986"
/clone_1b="NT2RP4"
/cell_type="teratocarcinoma"
/note="Vector: PME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 222 a 249 c 292 g 190 t 7 others
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 9; Length 960;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGCGCTGTAAACAGTA 18
|||||
DB 467 GCGCGCTGTAAACAGTA 450

RESULT 5

LOCUS BR337900 964 bp mRNA linear EST 22-NOV-2000
DEFINITION 602035724F1 NCI-CGAP Brn64 Homo sapiens cDNA clone IMAGE:4183901
5', mRNA sequence.
ACCESSION BR337900
VERSION BR337900.1 GI:11284275
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 964)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14W500 row: 0 column: 06
High quality sequence stop: 672.
Location/Qualifiers
1. 964

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="IMAGE:4183901"
/clone_1b="NCI-CGAP Brn64"
/tissue_type="gastroblastoma with EGFR amplification"

/lab_host="DH10B (71 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 259 a 252 c 295 g 158 t
ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 964;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGCGCTGTAAACAGTA 18
|||||
DB 206 GCGCGCTGTAAACAGTA 189

RESULT 6

LOCUS AA091280 239 bp mRNA linear EST 24-OCT-1996
DEFINITION cchm2408 seq.F Human fetal heart, lambda ZAP Express Homo sapiens
cDNA 5', mRNA sequence.
ACCESSION AA091280
VERSION AA091280.1 GI:1635864
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 239)
Liew, C.C.
cDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cllw@rics.bwh.harvard.edu
PCR PRIMERS
FORWARD: 5' GCCAAGCTCGAATTAACTCCTCAGTAACGG 3'
BACKWARD: 5' CCGATGATGTAAATACGACCTCATGTGGCG 3'
Seq primer: 5' GAATTAACCTCCTCAGTAACGG 3'.
Location/Qualifiers
1. 239

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="Human fetal heart, lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adapter-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

BASE COUNT 87 a 45 c 63 g 44 t
ORIGIN

Query Match 94.4%; Score 17; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGCGCTGTAAACAGT 17
|||||
DB 162 GCGCGCTGTAAACAGT 178

RESULT 7

LOCUS AM125499 384 bp mRNA linear EST 22-OCT-1999
DEFINITION UT-M-BH2.2-gsm-d-12-0-UT s1 NIH-BMAP_M.S3.2 Mus musculus cDNA clone
UT-M-BH2.2-gsm-d-12-0-UT 3', mRNA sequence.

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

AUTHORS
Garratt, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., D.
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., M.
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, E.
Thihsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

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Oligo-OT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA-No.

FEATURES

source

Location/Qualifiers
1. 539
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="01-M-CG0P-Dpz-c-07-0-01"
/clone_1lb="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not 1; Site 2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG_SEQ=None found"

BASE COUNT 121 a 158 c 124 g 136 t
ORIGIN

Query Match

Best Local Similarity 94.48; Score 16.4; DB 12; Length 539;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGC GGCTGTGAACAGTA 18
||| |||||
DB 295 GGCAGCTGTGAACAGTA 312

Search completed: June 22, 2003, 09:13:30
Job time : 1761 secs